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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/960,428

DATE: 03/06/2002
TIME: 12:56:31

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\03062002\I960428.raw

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    3  <110> APPLICANT: Roche Diagnostics GmbH
    5  <120> TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in
prokaryotic cells
    7  <130> FILE REFERENCE: 5272/00/
C-->  9  <140> CURRENT APPLICATION NUMBER: US/09/960,428
C--> 10  <141> CURRENT FILING DATE: 2001-09-21
   12  <160> NUMBER OF SEQ ID NOS: 22
   14  <170> SOFTWARE: PatentIn Ver. 2.1
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   17  <211> LENGTH: 38
   18  <212> TYPE: DNA
   19  <213> ORGANISM: Artificial Sequence
   21  <220> FEATURE:
   22  <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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   28  <211> LENGTH: 40
   29  <212> TYPE: DNA
   30  <213> ORGANISM: Artificial Sequence
   32  <220> FEATURE:
   33  <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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   38  <210> SEQ ID NO: 3
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   40  <212> TYPE: DNA
   41  <213> ORGANISM: Artificial Sequence
   43  <220> FEATURE:
   44  <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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   50  <211> LENGTH: 1716
   51  <212> TYPE: DNA
   52  <213> ORGANISM: Avian Myeloblastosis Virus
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   56  attgaccagt ggccccttcc tgaaggtaaa cttgtagcgc taacgcaatt agtggaaaaa  120
   57  gaattacagt taggacatat agaaccttca cttagttgct ggaacacacc tgtctttgtg  180
   58  atccggaagg cttccggtgtc ttatcgctta ttgcatgact tgcgcgctgt taacgctaag  240
   59  cttgttcctt ttgggcgt ccaacaggg gcgccggttc tctccgcgct ccgcgtggc    300
   60  tggcccctga tggtcctaga cctcaaggat tgcttctttt ctattcctct tgcggaacaa  360
   61  gatcgcgaag cttttgcatt tacgctcccc tctgtgaata accaggcccc cgctcgaaga  420
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63 gtgggtcaaa tacttgagcc cttgcgactc aagcacccat ctctgcgcat gttgcattat 540
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65 gttatcagta cattggaaag agccgggttc accatttcgc ctgataaggt ccagagggag 660
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67 gtagcagaac ccaggatagc caccttgtgg gatgttcaga agctggtggg gtcacttcag 780
68 tggcttcgcc cagcgctagg aatcccgcct cgactgatgg gcccctttta tgagcagtta 840
69 cgagggtcag atcctaacga ggcgagggaa tggaatctag acatgaaaat ggcctggaga 900
70 gagatcgtgc agctcagcac cactgctgcc ttggaacgat gggaccctgc cctgcctctg 960
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78 gtctggaggg aggggcccaag gtgggagata aaagaaatag ctgatttggg ggcaagtgta 1440
79 caacaactgg aagcacgcgc tgtggccatg gcacttctgc tgtggccgac aacgcccact 1500
80 aatgtagtga ctgactctgc gtttgttgcg aaaatgttac tcaagatggg gcaggaggga 1560
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82 gccgccgttc tccacgtgcg gagtcattct gaggtgccag ggttttttcac agaaggaaat 1680
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86 <211> LENGTH: 2574
87 <212> TYPE: DNA
88 <213> ORGANISM: Avian Myeloblastosis Virus
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92 attgaccagt ggcccccttcc tgaaggtaaa cttgtagcgc taacgcaatt agtggaaaaa 120
93 gaattacagt taggacatat agaaccttca cttagttgct ggaacacacc tgtctttgtg 180
94 atccggaagg cttccgggtc ttatcgctta ttgcatgact tgcgcgctgt taacgctaag 240
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96 tggcccctga tggtcctaga cctcaaggat tgcttctttt ctattcctct tgcggaacaa 360
97 gatcgcgaag cttttgcatt tacgctcccc tctgtgaata accaggcccc cgctcgaaga 420
98 ttccaatgga aggtcttgcc ccaagggatg acctgttctc ccactatctg tcagttgata 480
99 gtgggtcaaa tacttgagcc cttgcgactc aagcacccat ctctgcgcat gttgcattat 540
100 atggatgatc ttttgctagc cgcctcaagt catgatgggt tggaagcggc aggggaggag 600
101 gttatcagta cattggaaag agccgggttc accatttcgc ctgataaggt ccagagggag 660
102 cccggagtac aatatcttgg gtacaagtta ggcagtacgt atgtagcacc cgtaggcctg 720
103 gtagcagaac ccaggatagc caccttgtgg gatgttcaga agctggtggg gtcacttcag 780
104 tggcttcgcc cagcgctagg aatcccgcct cgactgatgg gcccctttta tgagcagtta 840
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106 gagatcgtgc agctcagcac cactgctgcc ttggaacgat gggaccctgc cctgcctctg 960
107 gaaggagcgg tcgctagatg tgaacagggg gcaataggggg tcctgggaca gggactgtcc 1020
108 acacacccaa ggccatgttt gtggttattc tccacccaac ccaccaaggc gtttactgct 1080
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110 ggcaaggagg ttgatatcct cctgttgcct gcatgctttc gggaggacct tccgctcccg 1200
111 gagggatcc tgttagccct taggggggttt gcaggaaaaa tcaggagtag tgacacgcca 1260
112 tctatttttg acattgcgcg tccactgcat gtttctctga aagtgagggt taccgaccac 1320
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115 caacaactgg aagcacgcgc tgtggccatg gcacttctgc tgtggccgac aacgcccact 1500
116 aatgtagtga ctgactctgc gtttgttgcg aaaatgttac tcaagatggg gcaggaggga 1560
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131 gagacagggg agtgggaaaa aggatggaac gtgctggtct ggggacgagg ttatgcagct 2460
132 gtgaaaaaca gggacactga taaggttatt tgggtaccct ctcgaaaagt taaaccggac 2520
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136 <211> LENGTH: 572
137 <212> TYPE: PRT
138 <213> ORGANISM: Avian Myeloblastosis Virus
140 <400> SEQUENCE: 6
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144 Thr Pro Val Trp Ile Asp Gln Trp Pro Leu Pro Glu Gly Lys Leu Val
145              20               25              30
147 Ala Leu Thr Gln Leu Val Glu Lys Glu Leu Gln Leu Gly His Ile Glu
148          35               40              45
150 Pro Ser Leu Ser Cys Trp Asn Thr Pro Val Phe Val Ile Arg Lys Ala
151      50               55              60
153 Ser Gly Ser Tyr Arg Leu Leu His Asp Leu Arg Ala Val Asn Ala Lys
154  65               70               75                  80
156 Leu Val Pro Phe Gly Ala Val Gln Gln Gly Ala Pro Val Leu Ser Ala
157               85               90              95
159 Leu Pro Arg Gly Trp Pro Leu Met Val Leu Asp Leu Lys Asp Cys Phe
160               100              105             110
162 Phe Ser Ile Pro Leu Ala Glu Gln Asp Arg Glu Ala Phe Ala Phe Thr
163          115              120             125
165 Leu Pro Ser Val Asn Asn Gln Ala Pro Ala Arg Arg Phe Gln Trp Lys
166      130              135             140
168 Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile Cys Gln Leu Ile
169 145              150             155             160
171 Val Gly Gln Ile Leu Glu Pro Leu Arg Leu Lys His Pro Ser Leu Arg
172               165              170             175
174 Met Leu His Tyr Met Asp Asp Leu Leu Leu Ala Ala Ser Ser His Asp
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175                 180                 185                 190
177 Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr Leu Glu Arg Ala
178             195                 200                 205
180 Gly Phe Thr Ile Ser Pro Asp Lys Val Gln Arg Glu Pro Gly Val Gln
181     210                 215                 220
183 Tyr Leu Gly Tyr Lys Leu Gly Ser Thr Tyr Val Ala Pro Val Gly Leu
184 225                 230                 235                 240
186 Val Ala Glu Pro Arg Ile Ala Thr Leu Trp Asp Val Gln Lys Leu Val
187             245                 250                 255
189 Gly Ser Leu Gln Trp Leu Arg Pro Ala Leu Gly Ile Pro Pro Arg Leu
190             260                 265                 270
192 Met Gly Pro Phe Tyr Glu Gln Leu Arg Gly Ser Asp Pro Asn Glu Ala
193             275                 280                 285
195 Arg Glu Trp Asn Leu Asp Met Lys Met Ala Trp Arg Glu Ile Val Gln
196     290                 295                 300
198 Leu Ser Thr Thr Ala Ala Leu Glu Arg Trp Asp Pro Ala Leu Pro Leu
199 305                 310                 315                 320
201 Glu Gly Ala Val Ala Arg Cys Glu Gln Gly Ala Ile Gly Val Leu Gly
202             325                 330                 335
204 Gln Gly Leu Ser Thr His Pro Arg Pro Cys Leu Trp Leu Phe Ser Thr
205             340                 345                 350
207 Gln Pro Thr Lys Ala Phe Thr Ala Trp Leu Glu Val Leu Thr Leu Leu
208     355                 360                 365
210 Ile Thr Lys Leu Arg Ala Ser Ala Val Arg Thr Phe Gly Lys Glu Val
211     370                 375                 380
213 Asp Ile Leu Leu Leu Pro Ala Cys Phe Arg Glu Asp Leu Pro Leu Pro
214 385                 390                 395                 400
216 Glu Gly Ile Leu Leu Ala Leu Arg Gly Phe Ala Gly Lys Ile Arg Ser
217             405                 410                 415
219 Ser Asp Thr Pro Ser Ile Phe Asp Ile Ala Arg Pro Leu His Val Ser
220             420                 425                 430
222 Leu Lys Val Arg Val Thr Asp His Pro Val Pro Gly Pro Thr Val Phe
223     435                 440                 445
225 Thr Asp Ala Ser Ser Ser Thr His Lys Gly Val Val Val Trp Arg Glu
226     450                 455                 460
228 Gly Pro Arg Trp Glu Ile Lys Glu Ile Ala Asp Leu Gly Ala Ser Val
229 465                 470                 475                 480
231 Gln Gln Leu Glu Ala Arg Ala Val Ala Met Ala Leu Leu Leu Trp Pro
232             485                 490                 495
234 Thr Thr Pro Thr Asn Val Val Thr Asp Ser Ala Phe Val Ala Lys Met
235     500                 505                 510
237 Leu Leu Lys Met Gly Gln Glu Gly Val Pro Ser Thr Ala Ala Ala Phe
238             515                 520                 525
240 Ile Leu Glu Asp Ala Leu Ser Gln Arg Ser Ala Met Ala Ala Val Leu
241     530                 535                 540
243 His Val Arg Ser His Ser Glu Val Pro Gly Phe Phe Thr Glu Gly Asn
244 545                 550                 555                 560
246 Asp Val Ala Asp Ser Gln Ala Thr Phe Gln Ala Tyr
247             565                 570
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249 <210> SEQ ID NO: 7
250 <211> LENGTH: 858
251 <212> TYPE: PRT
252 <213> ORGANISM: Avian Myeloblastosis Virus
254 <400> SEQUENCE: 7
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258 Thr Pro Val Trp Ile Asp Gln Trp Pro Leu Pro Glu Gly Lys Leu Val
259   20   25   30
261 Ala Leu Thr Gln Leu Val Glu Lys Glu Leu Gln Leu Gly His Ile Glu
262   35   40   45
264 Pro Ser Leu Ser Cys Trp Asn Thr Pro Val Phe Val Ile Arg Lys Ala
265   50   55   60
267 Ser Gly Ser Tyr Arg Leu Leu His Asp Leu Arg Ala Val Asn Ala Lys
268 65   70   75   80
270 Leu Val Pro Phe Gly Ala Val Gln Gln Gly Ala Pro Val Leu Ser Ala
271   85   90   95
273 Leu Pro Arg Gly Trp Pro Leu Met Val Leu Asp Leu Lys Asp Cys Phe
274   100   105   110
276 Phe Ser Ile Pro Leu Ala Glu Gln Asp Arg Glu Ala Phe Ala Phe Thr
277   115   120   125
279 Leu Pro Ser Val Asn Asn Gln Ala Pro Ala Arg Arg Phe Gln Trp Lys
280   130   135   140
282 Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile Cys Gln Leu Ile
283 145   150   155   160
285 Val Gly Gln Ile Leu Glu Pro Leu Arg Leu Lys His Pro Ser Leu Arg
286   165   170   175
288 Met Leu His Tyr Met Asp Asp Leu Leu Leu Ala Ala Ser Ser His Asp
289   180   185   190
291 Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr Leu Glu Arg Ala
292   195   200   205
294 Gly Phe Thr Ile Ser Pro Asp Lys Val Gln Arg Glu Pro Gly Val Gln
295   210   215   220
297 Tyr Leu Gly Tyr Lys Leu Gly Ser Thr Tyr Val Ala Pro Val Gly Leu
298 225   230   235   240
300 Val Ala Glu Pro Arg Ile Ala Thr Leu Trp Asp Val Gln Lys Leu Val
301   245   250   255
303 Gly Ser Leu Gln Trp Leu Arg Pro Ala Leu Gly Ile Pro Pro Arg Leu
304   260   265   270
306 Met Gly Pro Phe Tyr Glu Gln Leu Arg Gly Ser Asp Pro Asn Glu Ala
307   275   280   285
309 Arg Glu Trp Asn Leu Asp Met Lys Met Ala Trp Arg Glu Ile Val Gln
310   290   295   300
312 Leu Ser Thr Thr Ala Ala Leu Glu Arg Trp Asp Pro Ala Leu Pro Leu
313 305   310   315   320
315 Glu Gly Ala Val Ala Arg Cys Glu Gln Gly Ala Ile Gly Val Leu Gly
316   325   330   335
318 Gln Gly Leu Ser Thr His Pro Arg Pro Cys Leu Trp Leu Phe Ser Thr
319   340   345   350

VERIFICATION SUMMARY
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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date